Supplemental Material
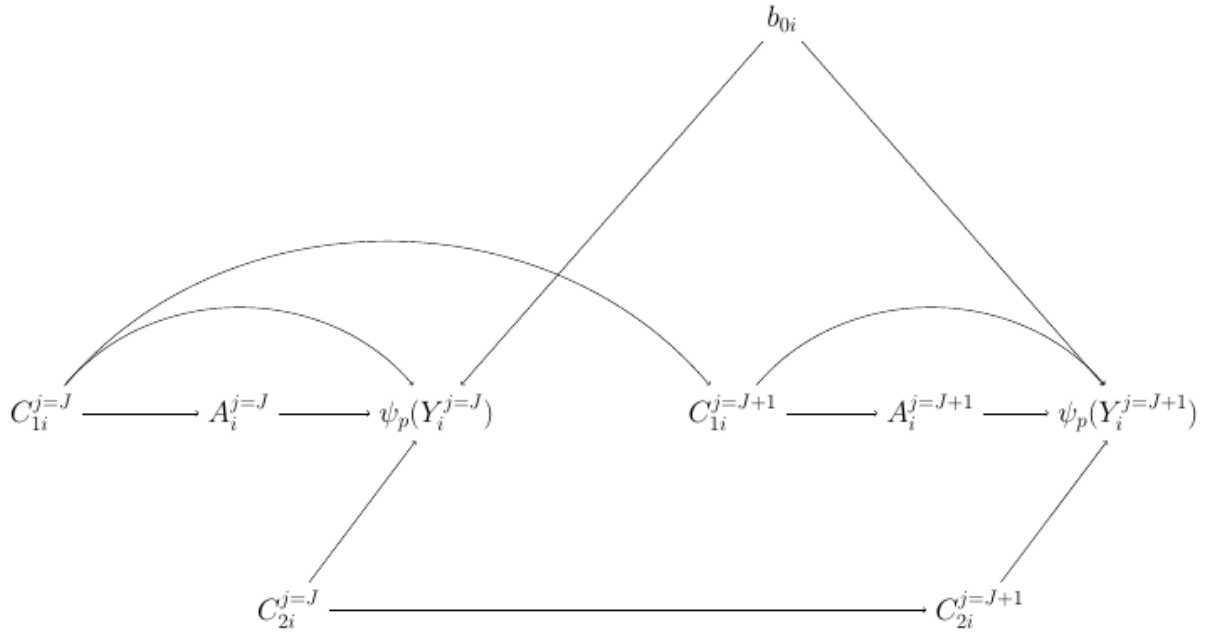
Beyond the Mean: Quantile Regression to Explore the Association of Air Pollution with Gene-Specific Methylation in the Normative Aging Study

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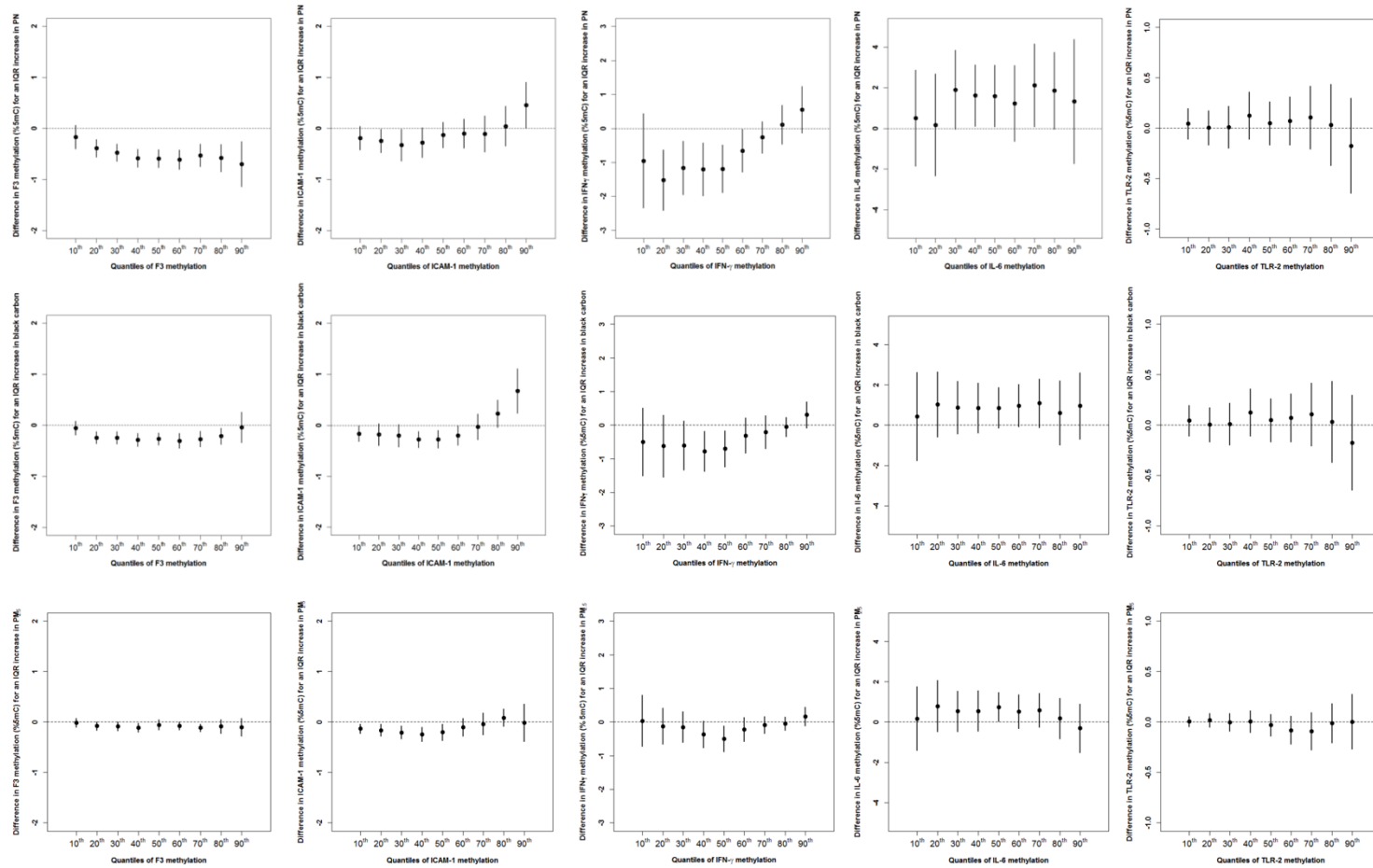
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Figure S1. Directed Acyclic Graph (DAG) at adjacent visits j=J and j=J+1. This DAG illustrates the relationships we assumed between the variables included in the regression models. A_i^j represents the 4-week moving average of air pollutant concentration before the jth visit of participant i. Y_i^j represents the ith participant gene-specific DNA methylation at visit j. $\psi_p(Y_i^j)$ is the pth quantile of the Y_{ij} distribution. C_{1i}^j and C_{2i}^j correspond to the potential confounding variables and risk factors of DNA methylation for participant i^{th} at visit j, respectively. b_{0i} represents the random intercept of participant i.

Figure S2. Sensitivity analyses restricted to never and former smokers: absolute difference in gene-specific methylation (expressed in %5mC with 95%CI) associated with an IQR increase in exposure (IQR=14,599 number per cm^3 for particle number, 0.26 $\mu g/m^3$ for $PM_{2.5}$ black carbon, and 3.4 $\mu g/m^3$ for $PM_{2.5}$ mass), according to deciles of the methylation distribution. In this secondary analysis, we considered only never and former smokers based on the time-varying smoking status variable. The analysis included 755 participants and 1,737 individual observations.

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